

RAW SEQUENCE LISTING ERROR REPORT



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Application Serial Number: 09/856,617A
Source: PCT09
Date Processed by STIC: 12/4/02

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FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

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Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name,
Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
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2011 South Clark Place, Arlington, VA 22202
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PCT09

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/856,617A

DATE: 12/04/2002
TIME: 13:50:11

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Output Set: N:\CRF4\12032002\I856617A.raw

3 <110> APPLICANT: KYOWA HAKKO KOGYO CO., LTD.,
5 <120> TITLE OF INVENTION: NOVEL POLYPEPTIDE
7 <130> FILE REFERENCE: 766.52
9 <140> CURRENT APPLICATION NUMBER: US 09/856,617A
10 <141> CURRENT FILING DATE: 2001-05-24
12 <150> PRIOR APPLICATION NUMBER: H10-332484
13 <151> PRIOR FILING DATE: 1998-11-24
15 <150> PRIOR APPLICATION NUMBER: H11-248442
16 <151> PRIOR FILING DATE: 1999-09-02
18 <160> NUMBER OF SEQ ID NOS: 18
19 <170> SOFTWARE: PatentIn Ver. 2.0

ERRORRED SEQUENCES

372 <210> SEQ ID NO: 2
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 374 <212> TYPE: DNA
 375 <213> ORGANISM: Mouse
 377 <220> FEATURE:
 378 <221> NAME/KEY: CDS
 379 <222> LOCATION: (107)..(4045)
 381 <400> SEQUENCE: 2
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 385 115
 386 Met Met Glu
 388 atc cag atg gac gag gga gga ggt gtg gtg gtg tac caa gac gac tac 163
 389 Ile Gln Met Asp Glu Gly Gly Val Val Val Tyr Gln Asp Asp Tyr
 390 5 10 15
 392 tgc tcg ggc tcg gtc atg tcg gag cgt gtg tcg ggc ctg gcg ggc tcc 211
 393 Cys Ser Gly Ser Val Met Ser Glu Arg Val Ser Gly Leu Ala Gly Ser
 394 20 25 30 35
 396 atc tac cgc gag ttc gag cgc ctc att cac tgc tat gac gag gag gtg 259
 397 Ile Tyr Arg Glu Phe Glu Arg Leu Ile His Cys Tyr Asp Glu Glu Val
 398 40 45 50
 400 gtc aag gag ctc atg ccg ctg gtg aac gtg ctg gag aac ctt gac 307
 401 Val Lys Glu Leu Met Pro Leu Val Val Asn Val Leu Glu Asn Leu Asp
 402 55 60 65
 404 tcg gtg ctg agc gag aac cag gag cac gag gtg gag ctg gag ctc cta 355
 405 Ser Val Leu Ser Glu Asn Gln Glu His Glu Val Glu Leu Glu Leu Leu
 406 70 75 80
 408 cgc gag gac aac gag cag ctg ctc acg caa tac gag cgc gag aag gca 403

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670	1125	1130	1135	
672	ggc aat ggg gtt gtc atc tcc atc ccc ttg act gag act gtg gtc ctg			3571
673	Gly Asn Gly Val Val Ile Ser Ile Pro Leu Thr Glu Thr Val Val Leu			
674	1140	1145	1150	1155
676	cat cga ggc cag ctc cta ggg ctc cga gcc aac aag aca tcc cca aca			3619
677	His Arg Gly Gln Leu Leu Gly Leu Arg Ala Asn Lys Thr Ser Pro Thr			
678	1160	1165	1170	
680	tct ggg gag ggg acc cgc cca ggg ggc atc atc cat gtg tat ggg gac			3667
681	Ser Gly Glu Gly Thr Arg Pro Gly Gly Ile Ile His Val Tyr Gly Asp			
682	1175	1180	1185	
684	gac agc agt gac aag gcc gcc agt agt ttc atc ccc tac tgc tcc atg			3715
685	Asp Ser Ser Asp Lys Ala Ala Ser Ser Phe Ile Pro Tyr Cys Ser Met			
686	1190	1195	1200	
688	gca cag gct cag ctt tgc ttc cat ggg cac cgt gat gct gtc aaa ttc			3763
689	Ala Gln Ala Gln Leu Cys Phe His Gly His Arg Asp Ala Val Lys Phe			
690	1205	1210	1215	
692	ttt gtc tct gtg cca gga aat gtg ctg gcc act ctc aat ggc agt gtg			3811
693	Phe Val Ser Val Pro Gly Asn Val Leu Ala Thr Leu Asn Gly Ser Val			
694	1220	1225	1230	1235
696	cta gac agc cca tca gag ggc cct ggg cct gct gca ccc gct gca gat			3859
697	Leu Asp Ser Pro Ser Glu Gly Pro Gly Pro Ala Ala Pro Ala Ala Asp			
698	1240	1245	1250	
700	gct gag ggc cag aag ttg aag aat gca ctg gtg ctg agt ggt ggt gaa			3907
701	Ala Glu Gly Gln Lys Leu Lys Asn Ala Leu Val Leu Ser Gly Gly Glu			
702	1255	1260	1265	
704	ggt tac att gac ttc cgt atc gga gac gga gag gat gat gaa act gag			3955
705	Gly Tyr Ile Asp Phe Arg Ile Gly Asp Gly Glu Asp Asp Glu Thr Glu			
706	1270	1275	1280	
708	gaa tgt gcc ggg gac gtg aac cag aca aag ccc tcg ttg tcc aag gct			4003
709	Glu Cys Ala Gly Asp Val Asn Gln Thr Lys Pro Ser Leu Ser Lys Ala			
710	1285	1290	1295	
E-->	712 gag cgc agc cac atc atc gtg tgg cag gtg tcc tac acc cct gag			
	Glu Arg Ser His Ile Ile Val Trp Gln Val Ser Tyr Thr Pro Glu			
	713 1300	1305	1310	
E-->	716 tgagaccctg tcctaacctga tgccaaactgt acataggacc ctacacctgct gcctccccgc			4102
E-->	718 ctgttccctg gggcagccag ttctgtccat cccctttaa cctctcaact tgcagcttt			4162
	720 gcctgaggtc cagcccttag ctgttagaga gg			4200
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2046	Met Ala Ala Gly Gly Asn Arg Asp Gly Glu Lys Arg Gly Ser Arg			
2047	1	5	10	15
2049	agc cag gcg gac tct ggc ttc ctg ggg ctg cgg ccg acc tcg gtg gat			99

4043 - Counted 4048

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Sq. 8

2115	275	280	285	
2117	gcc acc cag gag tcc gtg ttt cg ^g gag atg tgt gag ggc ctg ctg gag			915
2118	Ala Thr Gln Glu Ser Val Phe Arg Glu Met Cys Gly Leu Leu Glu			
2119	290	295	300	
2121	gag tct gat ggt gag gat gag cat gag gca ggc cgt gcc ggg cag cca			963
2122	Glu Ser Asp Gly Glu Asp Glu His Glu Ala Gly Arg Ala Gly Gln Pro			
2123	305	310	315	
2125	gag gct ggt gat ggg acc acc gag atc tca ccc act ggt gct gct ggt			1011
2126	Glu Ala Gly Asp Gly Thr Thr Glu Ile Ser Pro Thr Gly Ala Ala Gly			
2127	320	325	330	335
2129	cct gag aag agg atg gag aag aac acg gag cag cag cgg cgg cgg gag			1059
2130	Pro Glu Lys Arg Met Glu Lys Lys Thr Glu Gln Gln Arg Arg Arg Glu			
2131	340	345	350	
2133	aaa gct gct cgc aag ctg cgg gtg cag cag gct gca ctg agg gca gcc			1107
2134	Lys Ala Ala Arg Lys Leu Arg Val Gln Gln Ala Ala Leu Arg Ala Ala			
2135	355	360	365	
2137	cgg ctt cag cac caa gaa ctt ttc agg ctg cgt ggg atc aag gcc cag			1155
2138	Arg Leu Gln His Glu Leu Phe Arg Leu Arg Gly Ile Lys Ala Gln			
2139	370	375	380	
2141	gtg gcc cga agg ctg gca gaa ctg gca cgc cgg agg gag cag cgg cgc			1203
2142	Val Ala Arg Arg Leu Ala Glu Leu Ala Arg Arg Arg Glu Gln Arg Arg			
2143	385	390	395	
2145	ata cgg cga ctg gca gag gct gac aag ccc cga agg ctg gga cgg ctc			1251
2146	Ile Arg Arg Leu Ala Glu Ala Asp Lys Pro Arg Arg Leu Gly Arg Leu			
2147	400	405	410	415
2149	aag tac cag gct cct gac att gat gtg cag ctc agc tct gag ttg tct			1299
2150	Lys Tyr Gln Ala Pro Asp Ile Asp Val Gln Leu Ser Ser Glu Leu Ser			
2151	420	425	430	
2153	ggc tca ctc agg aca ctg aag cca gaa ggt cac att ctc cga gac agg			1347
2154	Gly Ser Leu Arg Thr Leu Lys Pro Glu Gly His Ile Leu Arg Asp Arg			
2155	435	440	445	
2157	tcc aag agc ttc cag aag aga aat atg att gag ccc cga gaa cga gcc			1395
2158	Phe Lys Ser Phe Gln Lys Arg Asn Met Ile Glu Pro Arg Glu Arg Ala			
2159	450	455	460	
2161	aag ttc aag cgc aaa tac aaa gtg aag ctg gtg gag aag cgg gcc tac			1443
2162	Lys Phe Lys Arg Lys Tyr Lys Val Lys Leu Val Glu Lys Arg Ala Tyr			
2163	465	470	475	
E-->	2165 cgt gag att cag ttg tag ctgtcagat g			
E-->	2166 Arg Glu Ile Gln Leu			
E-->	2167 480			
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2179	Asp Asp Tyr Cys Ser Gly Ser Val Met Ser Glu Arg Val Ser Gly Leu			
2180	20	25	30	

(1469) - Counted 1472

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Input Set : A:\SEQUENCE LISTING.txt
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Seq. 9

2329 Leu Val Gly Cys Ala Thr Arg Cys Asn Val Pro Arg Ser Asn Cys Ser
 2330 820 825 830
 2332 Ser Arg Gly Asp Thr Pro Val Leu Asp Lys Gly Gln Gly Asp Val Ala
 2333 835 840 845
 2335 Thr Thr Ala Asn Gly Lys Val Asn Pro Ser Gln Ser Thr Glu Glu Ala
 2336 850 855 860
 2338 Thr Glu Ala Thr Glu Val Pro Asp Pro Gly Pro Ser Glu Ser Glu Ala
 2339 865 870 875 880
 2341 Thr Thr Val Arg Pro Gly Pro Leu Thr Glu His Val Phe Thr Asp Pro
 2342 885 890 895
 2344 Ala Pro Thr Pro Ser Ser Ser Thr Gln Pro Ala Ser Glu Asn Gly Ser
 2345 900 905 910
 2347 Glu Ser Asn Gly Thr Ile Val Gln Pro Gln Val Glu Pro Ser Gly Glu
 2348 915 920 925
 2350 Leu Ser Thr Thr Ser Ser Ala Ala Pro Thr Met Trp Leu Gly Ala
 2351 930 935 940
 2353 Gln Asn Gly Trp Leu Tyr Val His Ser Ala Val Ala Asn Trp Lys Lys
 2354 945 950 955 960
 2356 Cys Leu His Ser Ile Lys Leu Lys Asp Ser Val Leu Ser Leu Val His
 2357 965 970 975
 2359 Val Lys Gly Arg Val Leu Val Ala Leu Ala Asp Gly Thr Leu Ala Ile
 2360 980 985 990
 2362 Phe His Arg Gly Glu Asp Gly Gln Trp Asp Leu Ser Asn Tyr His Leu
 2363 995 1000 1005
 2365 Met Asp Leu Gly His Pro His His Ser Ile Arg Cys Met Ala Val Val
 2366 1010 1015 1020
 2368 Asn Asp Arg Val Trp Cys Gly Tyr Lys Asn Lys Val His Val Ile Gln
 E--> 2369 {025 1030 1035 1040
 2371 Pro Lys Thr Met Gln Ile Glu Lys Ser Phe Asp Ala His Pro Arg Arg
 2372 1045 1050 1055
 2374 Glu Ser Gln Val Arg Gln Leu Ala Trp Ile Gly Asp Gly Val Trp Val
 2375 1060 1065 1070
 2377 Ser Ile Arg Leu Asp Ser Thr Leu Arg Leu Tyr His Ala His Thr His
 2378 1075 1080 1085
 2380 Gln His Leu Gln Asp Val Asp Ile Glu Pro Tyr Val Ser Lys Met Leu
 2381 1090 1095 1100
 2383 Gly Thr Gly Lys Leu Gly Phe Ser Phe Val Arg Ile Thr Ala Leu Leu
 E--> 2384 {105 1110 1115 1120
 2386 Ile Ala Gly Asn Arg Leu Trp Val Gly Thr Gly Asn Gly Val Val Ile
 2387 1125 1130 1135
 2389 Ser Ile Pro Leu Thr Glu Thr Val Val Leu His Arg Gly Gln Leu Leu
 2390 1140 1145 1150
 2392 Gly Leu Arg Ala Asn Lys Thr Ser Pro Thr Ser Gly Glu Gly Thr Arg
 2393 1155 1160 1165
 2395 Pro Gly Gly Ile Ile His Val Tyr Gly Asp Asp Ser Ser Asp Lys Ala
 2396 1170 1175 1180
 2398 Ala Ser Ser Phe Ile Pro Tyr Cys Ser Met Ala Gln Ala Gln Leu Cys
 E--> 2399 \185 1190 1195 1200
 2401 Phe His Gly His Arg Asp Ala Val Lys Phe Phe Val Ser Val Pro Gly

old, with the first part of the sequence removed

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2402 1205 1210 1215
2404 Asn Val Leu Ala Thr Leu Asn Gly Ser Val Leu Asp Ser Pro Ser Glu
2405 1220 1225 1230
2407 Gly Pro Gly Pro Ala Ala Pro Ala Ala Asp Ala Glu Gly Gln Lys Leu
2408 1235 1240 1245
2410 Lys Asn Ala Leu Val Leu Ser Gly Gly Glu Gly Tyr Ile Asp Phe Arg
2411 1250 1255 1260
2413 Ile Gly Asp Gly Glu Asp Asp Glu Thr Glu Glu Cys Ala Gly Asp Val
E--> 2414 1265 1270 1275 1280
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2417 1285 1290 1295
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2435 Ala Gly Ser Ile Tyr Arg Glu Phe Glu Arg Leu Ile His Cys Tyr Asp
2436 35 40 45
2438 Glu Glu Val Val Lys Glu Leu Met Pro Leu Val Val Asn Val Leu Glu
2439 50 55 60
2441 Asn Leu Asp Ser Val Leu Ser Glu Asn Gln Glu His Glu Val Glu Leu
2442 65 70 75 80
2444 Glu Leu Leu Arg Glu Asp Asn Glu Gln Leu Leu Thr Gln Tyr Glu Arg
2445 85 90 95
2447 Glu Lys Ala Leu Arg Lys Gln Ala Glu Glu Lys Phe Ile Glu Phe Glu
2448 100 105 110
2450 Asp Ala Leu Glu Gln Glu Lys Glu Leu Gln Ile Gln Val Glu His
2451 115 120 125
2453 Tyr Glu Phe Gln Thr Arg Gln Leu Glu Leu Lys Ala Lys Asn Tyr Ala
2454 130 135 140
2456 Asp Gln Ile Ser Arg Leu Glu Glu Arg Glu Ser Glu Met Lys Lys Glu
2457 145 150 155 160
2459 Tyr Asn Ala Leu His Gln Arg His Thr Glu Met Ile Gln Thr Tyr Val
2460 165 170 175
2462 Glu His Ile Glu Arg Ser Lys Met Gln Gln Val Gly Gly Ser Gly Gln
2463 180 185 190
2465 Thr Glu Ser Ser Leu Pro Gly Arg Ser Pro Arg Gln Ser Trp Arg Lys
2466 195 200 205
2468 Ser Arg Lys Glu Arg Pro Thr Ser Leu Asn Val Phe Pro Leu Ala Asp
2469 210 215 220
2471 Gly Met Cys Pro Asn Asp Glu Met Ser Glu Ser Gly Gln Ser Ser Ala
2472 225 230 235 240
2474 Ala Ala Thr Pro Ser Thr Gly Thr Lys Ser Asn Thr Pro Thr Ser

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Input Set : A:\SEQUENCE LISTING.txt
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Seq.10

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 2627 Lys Ser Phe Asp Ala His Pro Arg Arg Glu Ser Gln Val Arg Gln Leu
 2628 1060 1065 1070
 2630 Ala Trp Ile Gly Asp Gly Val Trp Val Ser Ile Arg Leu Asp Ser Thr
 2631 1075 1080 1085
 2633 Leu Arg Leu Tyr His Ala His Thr His Gln His Leu Gln Asp Val Asp
 2634 1090 1095 1100
 2636 Ile Glu Pro Tyr Val Ser Lys Met Leu Gly Thr Gly Lys Leu Gly Phe
 E--> 2637 |105 1110 1115 1120
 2639 Ser Phe Val Arg Ile Thr Ala Leu Leu Ile Ala Gly Asn Arg Leu Trp
 2640 1125 1130 1135
 2642 Val Gly Thr Gly Asn Gly Val Val Ile Ser Ile Pro Leu Thr Glu Thr
 2643 1140 1145 1150
 2645 Val Val Leu His Arg Gly Gln Leu Leu Gly Leu Arg Ala Asn Lys Thr
 2646 1155 1160 1165
 2648 Ser Pro Thr Ser Gly Glu Gly Thr Arg Pro Gly Gly Ile Ile His Val
 2649 1170 1175 1180
 2651 Tyr Gly Asp Asp Ser Ser Asp Lys Ala Ala Ser Ser Phe Ile Pro Tyr
 E--> 2652 |185 1190 1195 1200
 2654 Cys Ser Met Ala Gln Ala Gln Leu Cys Phe His Gly His Arg Asp Ala
 2655 1205 1210 1215
 2657 Val Lys Phe Phe Val Ser Val Pro Gly Asn Val Leu Ala Thr Leu Asn
 2658 1220 1225 1230
 2660 Gly Ser Val Leu Asp Ser Pro Ser Glu Gly Pro Gly Pro Ala Ala Pro
 2661 1235 1240 1245
 2663 Ala Ala Asp Ala Glu Gly Gln Lys Leu Lys Asn Ala Leu Val Leu Ser
 2664 1250 1255 1260
 2666 Gly Gly Glu Gly Tyr Ile Asp Phe Arg Ile Gly Asp Gly Glu Asp Asp
 E--> 2667 |265 1270 1275 1280
 2669 Glu Thr Glu Glu Cys Ala Gly Asp Val Asn Gln Thr Lys Pro Ser Leu
 2670 1285 1290 1295
 2672 Ser Lys Ala Glu Arg Ser His Ile Ile Val Trp Gln Val Ser Tyr Thr
 2673 1300 1305 1310
 2675 Pro Glu
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 2688 Asp Asp Tyr Cys Ser Gly Ser Val Met Ser Glu Arg Val Ser Gly Leu
 2689 20 25 30
 2691 Ala Gly Ser Ile Tyr Arg Glu Phe Glu Arg Leu Ile His Cys Tyr Asp
 2692 35 40 45
 2694 Glu Glu Val Val Lys Glu Leu Met Pro Leu Val Val Asn Val Leu Glu
 2695 50 55 60

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Seq. 11

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 2848 865 870 875 880
 2850 Thr Thr Ala Asn Gly Lys Val Asn Pro Ser Gln Ser Thr Glu Glu Ala
 2851 885 890 895
 2853 Thr Glu Ala Thr Glu Val Pro Asp Pro Gly Pro Ser Glu Ser Glu Ala
 2854 900 905 910
 2856 Thr Thr Val Arg Pro Gly Pro Leu Thr Glu His Val Phe Thr Asp Pro
 2857 915 920 925
 2859 Ala Pro Thr Pro Ser Ser Ser Thr Gln Pro Ala Ser Glu Asn Gly Ser
 2860 930 935 940
 2862 Glu Ser Asn Gly Thr Ile Val Gln Pro Gln Val Glu Pro Ser Gly Glu
 2863 945 950 955 960
 2865 Leu Ser Thr Thr Thr Ser Ser Ala Ala Pro Thr Met Trp Leu Gly Ala
 2866 965 970 975
 2868 Gln Asn Gly Trp Leu Tyr Val His Ser Ala Val Ala Asn Trp Lys Lys
 2869 980 985 990
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 2872 995 1000 1005
 2874 Val Lys Gly Arg Val Leu Val Ala Leu Ala Asp Gly Thr Leu Ala Ile
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 2881 1045 1050 1055
 2883 Asn Asp Arg Val Trp Cys Gly Tyr Lys Asn Lys Val His Val Ile Gln
 2884 1060 1065 1070
 2886 Pro Lys Thr Met Gln Ile Glu Lys Ser Phe Asp Ala His Pro Arg Arg
 2887 1075 1080 1085
 2889 Glu Ser Gln Val Arg Gln Leu Ala Trp Ile Gly Asp Gly Val Trp Val
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 2892 Ser Ile Arg Leu Asp Ser Thr Leu Arg Leu Tyr His Ala His Thr His
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 2896 1125 1130 1135
 2898 Gly Thr Gly Lys Leu Gly Phe Ser Phe Val Arg Ile Thr Ala Leu Leu
 2899 1140 1145 1150
 2901 Ile Ala Gly Asn Arg Leu Trp Val Gly Thr Gly Asn Gly Val Val Ile
 2902 1155 1160 1165
 2904 Ser Ile Pro Leu Thr Glu Thr Val Val Leu His Arg Gly Gln Leu Leu
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 2907 Gly Leu Arg Ala Asn Lys Thr Ser Pro Thr Ser Gly Glu Gly Thr Arg
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 2913 Ala Ser Ser Phe Ile Pro Tyr Cys Ser Met Ala Gln Ala Gln Leu Cys
 2914 1220 1225 1230
 2916 Phe His Gly His Arg Asp Ala Val Lys Phe Phe Val Ser Val Pro Gly

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2917 1235 1240 1245
 2919 Asn Val Leu Ala Thr Leu Asn Gly Ser Val Leu Asp Ser Pro Ser Glu
 2920 1250 1255 1260
 2922 Gly Pro Gly Pro Ala Ala Pro Ala Asp Ala Glu Gly Gln Lys Leu
 E--> 2923 1265 1270 1275 1280
 2925 Lys Asn Ala Leu Val Leu Ser Gly Gly Glu Gly Tyr Ile Asp Phe Arg
 2926 1285 1290 1295
 2928 Ile Gly Asp Gly Glu Asp Asp Glu Thr Glu Glu Cys Ala Gly Asp Val
 2929 1300 1305 1310
 2931 Asn Gln Thr Lys Pro Ser Leu Ser Lys Ala Glu Arg Ser His Ile Ile
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 2951 35 40 45
 2953 Glu Glu Val Val Lys Glu Leu Met Pro Leu Val Val Asn Val Leu Glu
 2954 50 55 60
 2956 Asn Leu Asp Ser Val Leu Ser Glu Asn Gln Glu His Glu Val Glu Leu
 2957 65 70 75 80
 2959 Glu Leu Leu Arg Glu Asp Asn Glu Gln Leu Leu Thr Gln Tyr Glu Arg
 2960 85 90 95
 2962 Glu Lys Ala Leu Arg Lys Gln Ala Glu Glu Lys Phe Ile Glu Phe Glu
 2963 100 105 110
 2965 Asp Ala Leu Glu Gln Glu Lys Glu Leu Gln Ile Gln Val Glu His
 2966 115 120 125
 2968 Tyr Glu Phe Gln Thr Arg Gln Leu Glu Leu Lys Ala Lys Asn Tyr Ala
 2969 130 135 140
 2971 Asp Gln Ile Ser Arg Leu Glu Glu Arg Glu Ser Glu Met Lys Lys Glu
 2972 145 150 155 160
 2974 Tyr Asn Ala Leu His Gln Arg His Thr Glu Met Ile Gln Thr Tyr Val
 2975 165 170 175
 2977 Glu His Ile Glu Arg Ser Lys Met Gln Gln Val Gly Gly Ser Gly Gln
 2978 180 185 190
 2980 Thr Glu Ser Ser Leu Pro Gly Arg Arg Lys Glu Arg Pro Thr Ser Leu
 2981 195 200 205
 2983 Asn Val Phe Pro Leu Ala Asp Gly Met Val Arg Ala Gln Met Gly Gly
 2984 210 215 220
 2986 Lys Leu Val Pro Ala Gly Asp His Trp His Leu Ser Asp Leu Gly Gln
 2987 225 230 235 240
 2989 Leu Gln Ser Ser Ser Tyr Gln Cys Pro Asn Asp Glu Met Ser Glu

RAW SEQUENCE LISTING
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DATE: 12/04/2002
TIME: 13:50:11

Input Set : A:\SEQUENCE LISTING.txt
Output Set: N:\CRF4\12032002\I856617A.raw

Seq. 12

E--> 3137 025	1030	1035	1040	
3139 Asp Leu Gly His Pro His His Ser Ile Arg Cys Met Ala Val Val Asn				
3140	1045	1050	1055	
3142 Asp Arg Val Trp Cys Gly Tyr Lys Asn Lys Val His Val Ile Gln Pro				
3143	1060	1065	1070	
3145 Lys Thr Met Gln Ile Glu Lys Ser Phe Asp Ala His Pro Arg Arg Glu				
3146	1075	1080	1085	
3148 Ser Gln Val Arg Gln Leu Ala Trp Ile Gly Asp Gly Val Trp Val Ser				
3149	1090	1095	1100	
3151 Ile Arg Leu Asp Ser Thr Leu Arg Leu Tyr His Ala His Thr His Gln				
E--> 3152 105	1110	1115	1120	
3154 His Leu Gln Asp Val Asp Ile Glu Pro Tyr Val Ser Lys Met Leu Gly				
3155	1125	1130	1135	
3157 Thr Gly Lys Leu Gly Phe Ser Phe Val Arg Ile Thr Ala Leu Leu Ile				
3158	1140	1145	1150	
3160 Ala Gly Asn Arg Leu Trp Val Gly Thr Gly Asn Gly Val Val Ile Ser				
3161	1155	1160	1165	
3163 Ile Pro Leu Thr Glu Thr Val Val Leu His Arg Gly Gln Leu Leu Gly				
3164	1170	1175	1180	
3166 Leu Arg Ala Asn Lys Thr Ser Pro Thr Ser Gly Glu Gly Thr Arg Pro				
E--> 3167 185	1190	1195	1200	
3169 Gly Gly Ile Ile His Val Tyr Gly Asp Asp Ser Ser Asp Lys Ala Ala				
3170	1205	1210	1215	
3172 Ser Ser Phe Ile Pro Tyr Cys Ser Met Ala Gln Ala Gln Leu Cys Phe				
3173	1220	1225	1230	
3175 His Gly His Arg Asp Ala Val Lys Phe Phe Val Ser Val Pro Gly Asn				
3176	1235	1240	1245	
3178 Val Leu Ala Thr Leu Asn Gly Ser Val Leu Asp Ser Pro Ser Glu Gly				
3179	1250	1255	1260	
3181 Pro Gly Pro Ala Ala Pro Ala Ala Asp Ala Glu Gly Gln Lys Leu Lys				
E--> 3182 265	1270	1275	1280	
3184 Asn Ala Leu Val Leu Ser Gly Gly Glu Gly Tyr Ile Asp Phe Arg Ile				
3185	1285	1290	1295	
3187 Gly Asp Gly Glu Asp Asp Glu Thr Glu Glu Cys Ala Gly Asp Val Asn				
3188	1300	1305	1310	
3190 Gln Thr Lys Pro Ser Leu Ser Lys Ala Glu Arg Ser His Ile Ile Val				
3191	1315	1320	1325	
3193 Trp Gln Val Ser Tyr Thr Pro Glu				
3194	1330	1335		
3285 <210> SEQ ID NO: 14				
3286 <211> LENGTH: 1508				
3287 <212> TYPE: PRT				
3288 <213> ORGANISM: Mouse				
3290 <400> SEQUENCE: 14				
3291 Met Met Ala Gly Glu Gly Ser Thr Ile Thr Ser Arg Ile Lys Asn Leu				
3292	1	5	10	15
3294 Leu Arg Ser Pro Ser Ile Lys Leu Arg Arg Ser Lys Ala Gly Asn Arg				
3295	20	25	30	
3297 Arg Glu Asp Leu Ser Ser Lys Val Thr Leu Glu Lys Val Leu Gly Val				

RAW SEQUENCE LISTING

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Input Set : A:\SEQUENCE LISTING.txt
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Seq. 14

3445	820	825	830
3447	Met Ser Arg Ala Gln Glu Thr Met Glu Tyr Leu Asp Pro Ala Pro Val		
3448	835	840	845
3450	Ala Asn Thr Gly Pro Lys Arg Arg Gly Arg Trp Ala Gln Pro Gly Val		
3451	850	855	860
3453	Glu Leu Ser Val Arg Ser Met Leu Asp Leu Arg Gln Ile Glu Thr Leu		
3454	865	870	875
3456	Ala Pro Ser Pro Arg Gly Pro Ser Gln Asp Ser Leu Ala Val Ser Pro		
3457	885	890	895
3459	Ala Gly Pro Gly Lys His Gly Pro Gln Ala Pro Glu Leu Ser Cys Val		
3460	900	905	910
3462	Ser Gln Asn Glu Arg Ala Pro Arg Leu Gln Thr Ser Gln Pro Cys Ser		
3463	915	920	925
3465	Cys Pro Asp Ile Ile Gln Leu Leu Ser Gln Glu Gly Val Phe Ala		
3466	930	935	940
3468	Gln Asp Leu Glu Pro Ala Pro Ile Glu Asp Gly Ile Val Tyr Pro Glu		
3469	945	950	955
3471	Pro Ser Asp Ser Pro Thr Met Asp Thr Ser Ala Phe Gln Val Gln Ala		
3472	965	970	975
3474	Pro Thr Gly Gly Ser Leu Gly Arg Met Tyr Pro Gly Ser Arg Gly Ser		
3475	980	985	990
3477	Glu Lys His Ser Pro Asp Ser Ala Cys Ser Val Asp Tyr Ser Ser Ser		
3478	995	1000	1005
3480	Arg Leu Ser Ser Pro Glu His Pro Asn Glu Asp Ser Glu Ser Thr Glu		
3481	1010	1015	1020
3483	Pro Leu Ser Val Asp Gly Ile Ser Ser Asp Leu Glu Glu Pro Ala Glu		
E--> 3484 025	1030	1035	1040
3486	Gly Asp Glu Asp Glu Glu Glu Gly Gly Thr Gly Leu Cys Gly Leu		
3487	1045	1050	1055
3489	Gln Glu Gly Gly Pro Arg Thr Pro Asp Gln Glu Gln Phe Leu Lys Gln		
3490	1060	1065	1070
3492	Leu Phe Glu Thr Leu Ala Asn Gly Thr Ala Pro Gly Gly Pro Ala Arg		
3493	1075	1080	1085
3495	Val Leu Glu Arg Thr Glu Ser Arg Ser Ile Ser Ser Arg Phe Leu Leu		
3496	1090	1095	1100
3498	Gln Val Gln Thr Leu Pro Leu Arg Glu Pro Ser Leu Ser Ser Ser Gly		
E--> 3499 105	1110	1115	1120
3501	Leu Ala Leu Thr Ser Arg Pro Asp Gln Val Ser Gln Val Ser Gly Glu		
3502	1125	1130	1135
3504	Gln Leu Lys Gly Ser Gly Ala Thr Pro Pro Gly Ala Pro Pro Glu Met		
3505	1140	1145	1150
3507	Glu Pro Ser Ser Gly Asn Ser Gly Pro Lys Gln Val Ala Pro Val Leu		
3508	1155	1160	1165
3510	Leu Thr Arg Arg Arg Asn Asn Leu Asp Asn Ser Trp Ala Ser Lys Lys		
3511	1170	1175	1180
3513	Met Ala Ala Thr Arg Pro Leu Ala Gly Leu Gln Lys Ala Gln Ser Val		
E--> 3514 185	1190	1195	1200
3516	His Ser Leu Val Pro Gln Asp Glu Val Pro Ser Ser Arg Pro Leu Leu		
3517	1205	1210	1215

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/856,617A

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Input Set : A:\SEQUENCE LISTING.txt
 Output Set: N:\CRF4\12032002\I856617A.raw

3519 Phe Arg Glu Ala Glu Thr Gln Gly Ser Leu Gly Ser Leu Pro Gln Ala
 3520 1220 1225 1230
 3522 Gly Gly Cys Ser Ser Gln Pro His Ser Tyr Gln Asn His Thr Thr Ser
 3523 1235 1240 1245
 3525 Ser Met Ala Lys Leu Ala Arg Ser Ile Ser Val Gly Glu Asn Pro Gly
 3526 1250 1255 1260
 3528 Leu Ala Thr Glu Pro Gln Ala Pro Ala Pro Ile Arg Ile Ser Pro Phe
E--> 3529 | 265 1270 1275 1280
 3531 Asn Lys Leu Ala Leu Pro Ser Arg Ala His Leu Val Leu Asp Ile Pro
 3532 1285 1290 1295
 3534 Lys Pro Leu Pro Asp Arg Pro Thr Leu Thr Thr Phe Ser Pro Val Ser
 3535 1300 1305 1310
 3537 Lys Gly Leu Thr His Asn Glu Thr Glu Gln Ser Gly Pro Leu Arg Glu
 3538 1315 1320 1325
 3540 Pro Arg Lys Ala His Thr Thr Val Glu Lys His Ser Cys Leu Gly Glu
 3541 1330 1335 1340
 3543 Gly Thr Thr His Lys Ser Arg Thr Glu Cys Gln Ala Tyr Pro Gly Pro
E--> 3544 | 345 1350 1355 1360
 3546 Asn His Pro Cys Arg Gln Gln Leu Pro Val Asn Asn Leu Leu Gln Ala
 3547 1365 1370 1375
 3549 Glu Ser Leu Gln Pro Leu Ser Pro Glu Lys Thr Arg Asn Pro Val Glu
 3550 1380 1385 1390
 3552 Ser Ser Arg Pro Gly Val Ala Leu Ser Gln Asp Ser Glu Leu Ala Leu
 3553 1395 1400 1405
 3555 Ser Leu Gln Gln Cys Glu Gln Leu Val Ala Glu Leu Gln Gly Asn Val
 3556 1410 1415 1420
 3558 Arg Gln Ala Val Glu Leu Tyr Arg Ala Val Thr Ser Cys Lys Thr Pro
E--> 3559 | 425 1430 1435 1440
 3561 Ser Ala Glu Gln Ser His Ile Thr Arg Leu Leu Arg Asp Thr Phe Ser
 3562 1445 1450 1455
 3564 Pro Val Arg Gln Glu Leu Glu Val Leu Ala Gly Ala Val Leu Ser Ser
 3565 1460 1465 1470
 3567 Pro Gly Gly Ser Pro Gly Ala Val Ala Ala Glu Gln Thr Gln Ala Leu
 3568 1475 1480 1485
 3570 Leu Glu Gln Tyr Ser Glu Leu Leu Leu Arg Ala Val Glu Arg Arg Met
 3571 1490 1495 1500
 3573 Glu Arg Arg Leu
E--> 3574 | 505
 3730 <210> SEQ ID NO: 17
 3731 <211> LENGTH: 27
 3732 <212> TYPE: DNA
 3733 <213> ORGANISM: Artificial Sequence
 3735 <220> FEATURE:
 3736 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
 3738 <400> SEQUENCE: 17
E--> 3739 tagatatcgc cttgaaacaa gagaaga → place here
 3740 (2)
 3743 <210> SEQ ID NO: 18
 3744 <211> LENGTH: 31

RAW SEQUENCE LISTING

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Input Set : A:\SEQUENCE LISTING.txt
Output Set: N:\CRF4\12032002\I856617A.raw

3745 <212> TYPE: DNA
3746 <213> ORGANISM: Artificial Sequence
3748 <220> FEATURE:
3749 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
3751 <400> SEQUENCE: 18
3752 atgaattctc agttgttctt tgtgacactg a 31

E--> 3753 1 / 142 - delete

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/856,617A

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Input Set : A:\SEQUENCE LISTING.txt

Output Set: N:\CRF4\12032002\I856617A.raw

L:712 M:254 E: No. of Bases conflict, LENGTH:Input:4043 Counted:4048 SEQ:2
M:254 Repeated in SeqNo=2
L:2165 M:254 E: No. of Bases conflict, LENGTH:Input:1469 Counted:1472 SEQ:8
L:2167 M:252 E: No. of Seq. differs, <211> LENGTH:Input:1469 Found:1472 SEQ:8
L:2369 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:9
M:332 Repeated in SeqNo=9
L:2622 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:10
M:332 Repeated in SeqNo=10
L:2878 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:11
M:332 Repeated in SeqNo=11
L:3137 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:12
M:332 Repeated in SeqNo=12
L:3484 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:14
M:332 Repeated in SeqNo=14
L:3739 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:27 SEQ:17
L:3753 M:254 E: No. of Bases conflict, LENGTH:Input:142 Counted:32 SEQ:18
L:3753 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:3753 M:252 E: No. of Seq. differs, <211> LENGTH:Input:31 Found:32 SEQ:18